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Distinct molecular signature of murine fetal liver and adult hematopoietic stem cells identifies novel regulators of hematopoietic stem cell function

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Abstract

During ontogeny, fetal liver (FL) acts as a major site for hematopoietic stem cell (HSC) maturation and expansion, while HSCs in the adult bone marrow (ABM) are largely quiescent. HSCs in the FL possess faster repopulation capacity as compared with ABM HSCs. However, the molecular mechanism regulating the greater self-renewal potential of FL HSCs has not yet extensively been assessed. Recently, we published RNA-sequencing based gene expression analysis on FL HSCs from 14.5 day mouse embryo (E14.5) in comparison to the ABM HSCs. We reanalyzed this data to identify key transcriptional regulators that play important roles in the expansion of HSCs during development. The comparison of FL E14.5 with ABM HSCs identified more than 1400 differentially expressed genes. More than 200 genes were shortlisted based on the GO annotation term “transcription”. By morpholino based knockdown studies in zebrafish, we assessed the function of 18 of these regulators, previously not associated with HSC proliferation. Our studies identified a previously unknown role for *tdg, uhrf1, uchl5, and ncoa1* in the emergence of definitive hematopoiesis in zebrafish. In conclusion, we demonstrate that identification of genes involved in transcriptional regulation differentially expressed between expanding FL HSCs and quiescent ABM HSCs, uncovers novel regulators of HSC function.

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Introduction

Long-term repopulating (LT) hematopoietic stem cells (HSCs) give rise to all the blood cell lineages throughout the lifespan of adult mammals [1]. One of the hallmark features of LT-HSCs is their ability to self-renew, which is governed by cell-intrinsic and -extrinsic factors. Due to different requirements of HSCs at different stages of development, the molecular determinants that regulate self-renewal are believed to be stage specific. During development, particularly in the fetal liver (FL), the main role of HSCs is to rapidly produce sufficient numbers of stem cells for the adult life while also giving rise to homeostatic levels of differentiated blood progeny. That the fetal liver is a pivotal organ where definitive HSCs expand [2], is reflected in the percentage of FL HSCs (30-35%) that are actively cycling. The increased proliferative potential of FL HSCs is evident from the studies wherein FL and ABM HSCs were grafted into irradiated hosts; resulting in a significantly faster HSC expansion from FL compared with ABM grafts [3]. By contrast, from 4 weeks after birth onwards more than 95% of the HSCs in adult bone marrow (ABM) are quiescent. Rare asymmetrical divisions allow the continuous supply of mature blood cells without losing primitive HSCs throughout the lifetime of an individual [4]. Differences in the cell surface antigen expression as well as global gene expression profiles have been described between FL HSCs and ABM HSCs [5-8].

Although it is well accepted that significant differences exist between the ability of FL and ABM HSCs to undergo symmetrical, self-renewing cell divisions without stem cell exhaustion, only few studies have addressed molecular pathways underlying these differences. For instance, the higher expansion potential of FL derived HSCs has been at least in part ascribed to Lin28b-let-7-Hmga2 mediated signaling, even if Lin28b cannot reactivate the FL HSC-like self-renewal properties in ABM HSCs [9]. By contrast, *Sox17*, which is required for the maintenance of FL HSC function, can also re-introduce the FL proliferative phenotype in ABM HSCs [10,11]. Interestingly, conditional deletion of *Lis1* in FL hematopoietic cells using *Vav-cre* was shown to cause defects HSC expansion and embryonic lethality; and a similar phenotype was observed after the deletion of *Lis1* in adult

HSC which caused decreased HSC self-renewal and differentiation in competitive repopulation assays [12,13].

Gaining further insights into the molecular regulators that support symmetrical self-renewal is of significant clinical relevance; in the setting of bone marrow failure syndromes, *ex vivo* HSC expansion methods and in the field of leukemogenesis. To uncover candidate molecular regulators for FL HSC self-renewal, we performed RNA-sequencing analysis to define the differences in the genome-wide transcriptome of HSCs from FL and ABM.

To investigate the functional role of differentially expressed genes for their importance in definitive hematopoiesis, we used zebrafish, *Danio Rerio*, as the model organism. In Zebrafish, definitive HSCs that support multi-lineage engraftment appear along the ventral wall of dorsal aorta, which is an equivalent of the AGM region and express *c-myb* and *runx1 [14,15]*. Several signaling pathways have been identified that regulate specification and development of HSCs in zebrafish, including Notch, Runx1, fibroblast growth factor, vascular endothelial growth factor, bone morphogenetic protein and Hedgehog [16-19]. These cellular and molecular mechanisms underlying the emergence or specification of these multipotent hematopoietic stem and progenitors cells (HSPCs) are largely conserved between mammals and zebrafish [16,20-22]. Hence, the easy accessibility to manipulate and visualize early stage embryos and the relatively high homology in the genetic regulation of hematopoiesis makes genetic screens in zebrafish a very useful method to interrogate in a semi high throughput manner the role of specific genes in hematopoiesis.

We used our earlier published RNASeq [23] data to identify 18 differentially expressed genes between E14.5 FL and ABM HSC that could be important regulators for HSC expansion. Morpholino anti-sense oligonucleotide (MO) knockdown technology was used to address their possible role in hematopoiesis. Our study identified 4 differentially expressed genes, with previously unknown function in HSC biology, to affect emergence of definitive hematopoiesis in zebrafish larvae.

Methods

Animals: Six to ten weeks old C57BL/6J-CD45.2 (Centre d'Elevage R. Janvier, Le Genest-St Isle, France, http://www.criver.com/) were bred and maintained in the animal facility at KU Leuven, Belgium. During the experiments, mice were maintained in isolator cages, fed with autoclaved acidified water, and irradiated food ad libitum. All the experimental procedures involving mice and Zebrafish were approved by the Institutional Animal Ethics Committee of KU Leuven.

Isolation of LT-HSC from bone marrow and fetal liver:

The isolation and purification of LT-HSC from murine FL E14.5 and ABM has been described in our pervious study [23].

RNA-sequencing and bioinformatics analysis:

RNA-seq data obtained from E14.5 FL and BM HSCs described in [23] were reanalyzed in a similar manner as previously described[23]. Unlike in our previous publication [23], the high quality reads were aligned to the mouse reference genome mm9 using SOAPaligner/SOAP2. Quality was checked for the alignment and later downstream analysis including gene annotation, gene expression, alternative splicing and novel transcript prediction was performed. The differential expression analysis of genes was performed using the R package DESeq[24] and differentially expressed genes were identified using the following thresholds: false discovery rate (FDR) ≤ 0.05 and log2 fold change ≥ 1.0. The gene-set enrichment test was then carried out to detect significantly enriched gene sets using Genecodis[25]. Sequencing data related to FL and BM HSC can be accessed via ArrayExpress database (http://www.ebi.ac.uk/arrayexpress) with accession number: E- MTAB-4034.

Quantitative RT-PCR:

For each replicate, we used three times 6 embryos that had been injected with MOs as well as uninjected controls 48 hour post-fertilization. 4-6 replicates were collected and RNA was extracted using the GenElute Mammalian Total RNA Miniprep Kit (Sigma-Aldrich) following

manufacturer's instructions. A DNase treatment was performed while the RNA was bound to the column using an On-Column DNaseI Digestion Set (Sigma-Aldrich). cDNA was synthetized using the SuperScript III First-Strand Synthesis SuperMix for qRT-PCR (Invitrogen) according to manufacture protocol. qRT-PCR was performed in a FrameStar 384 plate (4titude) using the Platinum SYBR Green qRT-PCR SuperMix-UDG (Invitrogen). Rox Reference Dye was added to the Platinum SYBR Green qPCR SuperMix-UDG in a concentration of 50 nM. A list of primers used for the qRT-PCR can be found in Table S1. We measured the transcript levels for the erythroid-specific gene *hbae1* and the myeloid-specific gene *lcp1*. Gene expression for different transcripts was calculated relative to *gapdh* as a housekeeping gene. Fold change was calculated relative to uninjected controls. The qRT-PCR was performed using ViiA7 Real-Time PCR System (Applied Biosystems).

For some genes, differentially expressed gene identified between ABM and E14.5 FL were analysed by qRT-PCR to confirm differential gene expression. RNA isolation and qRT-PCR was performed as previously described and list of primers used for the qRT-PCR can be found in Table S1. Gene expression for different transcripts was calculated relative to *β-actin* as a housekeeping gene.

Morpholino injection:

Zebrafish (Danio rerio) were bred, raised, and maintained according to Animal handling guidelines at KU Leuven. Embryos were incubated at 28.5°C and staged according to hours post-fertilization (hpf) and morphological features as published (Kimmel et al. 1995). For high throughput screening, double transgenic zebrafish with a DsRed reporter under the control of the *gata1* promoter (Tg(*gata1*:DsRed)) and EGFP reporter under the control of the *flk1* promoter (Tg(*flk1*:EGFP)) were used. Morpholino antisense oligonucleotides (MOs), targeting the translational initiation (starting codon) of candidate genes (Table S2), preventing protein translation, were obtained from Gene tools, LLC (OR, USA). For some genes we designed second MOs targeting the splice junction (Table S2)

MOs were injected at the 1-2 cell stage (70-100 embryos) with a starting concentration of

4ng/embryo. The concentration was increased to 5, 6, 7ng if there was no defect on blood flow (increase or decrease in DsRed (*gata1*) signal) and the concentration was decreased to 3, 2, 1.5ng if there was a defect in blood to identify the lowest concentration possible. Embryos were screened under fluorescence microscope at 48hr post microinjection and imaged using Zeiss Axio Imager microscope.

Whole-mount *in situ* hybridization (WISH):

WISH for *c-myb* and *runx1* expression was performed on uninjected and MO injected embryos at 36hpf as described previously[26]. In brief, *in situ* hybridization using DIG-labeled antisense riboprobes *runx1* and *c-myb* that were transcribed from linearized plasmid using T7 RNA polymerase (Roche). 36hpf embryos were fixed with 4% PFA overnight and permeabilized using ProteinaseK (1mg/ml) for 20 minute. Embryos were hybridized overnight in water bath at 68°C. After hybridization embryos were washed several times as previously described[26] and rinse in MABT (Maleic Acid buffer + 0.1% tween-20). Next, incubate embryos in blocking solution (1 part 10% Boehringer Mannheim Blocking reagent (BMB), 1 part lamb serum, 8 parts MAB) at RT for 2-3 hours. Hybridization was detected using anti-DIG antibody (Roche) coupled to alkaline phosphatase (AP). Embryos were washed by MABT (6 x 15 minutes) to remove excess of antibody. DIG antibody-alkaline phosphatase conjugate was detected using NBT/BCIP (Sigma). Stained embryos were mounted in 70% glycerol and imaged on an Olympus compound microscope with a camera.

Statistical analysis: The significance of difference was estimated by two-tailed Student's t-test. $p \leq 0.05$ was considered statistically significant.

Results

Genome-wide transcriptome analysis of fetal liver and adult bone marrow LT-HSCs

To define developmentally regulated differences in the transcriptome of extensively self-renewing FL HSCs and quiescent ABM HSCs, we re-analyzed RNA-seq obtained from HSCs derived from mouse FL and ABM as previously described [23]. LT-HSCs were isolated from E14.5 FL as $Lin^-Sca\text{-}1^+Mac\text{-}1^+CD150^+CD48^-$ cells, and from ABM HSCs as $Lin^-Sca\text{-}1^+c\text{-}kit^+ CD150^+CD48^-$ cells using FACS. RNA from all samples was amplified and subjected to 91 bp pair-end sequencing at Beijing Genomics Institute (BGI, Shenzhen). Raw sequencing reads that had been filtered into clean reads, were aligned to the reference genome sequence mm9 using SOAPaligner/SOAP2. Alignment data were then used to calculate the distribution of reads on reference genes/genome (Fig. S1A,B), and to obtain normalized expression values by calculating RPKM (Reads Per Kilobase of transcript per Million mapped reads) (Table S3). Pearson correlation between the biological replicates demonstrated that samples at each stage were highly correlated (Fig. S1C). Principal component analysis (PCA) showed that the FL HSC populations were distinct from ABM HSCs (Fig. 1A).

Next, we performed a pair-wise comparison between both FL E14.5 and adult BM HSCs to obtain differentially expressed genes (DEG) using the DESeq method (Fig. 1B and Table S4).[27] Because HSCs expand most abundantly at around E14.5, we compared the transcriptome of E14.5 FL HSCs with the transcriptome of ABM HSCs obtained from 8-week old mice, at which time HSCs are quiescent. We identified 1442 genes differentially expressed between E14.5 FL HSCs and the ABM derived HSCs ($Log_2FC \geq 1$ and $FDR \leq 0.05$)(703 genes were more highly expressed and 739 genes less expressed in FL HSCs compared with ABM HSCs) (Fig. 1B and Table S4).

We performed gene-set enrichment analysis for biological processes on genes differentially expressed between E14.5 FL and ABM (from our data published earlier [23]) using the web-based application, GeneCodis3 [25]. As expected, genes more highly expressed in FL E14.5 HSCs were enriched for biological processes related to cell proliferation, such as cell cycle,

cell division, mitosis, DNA replication and DNA repair (Fig. 1C). By contrast, genes more highly expressed in quiescent BM HSCs were enriched for biological processes related to the regulation of transcription, negative regulation of cell proliferation and antigen processing and presentation (Fig. 1D).

Shortlisting candidate genes from differentially expressed gene list for functional screen

To identify novel regulators of LT-HSC expansion, we selected genes annotated as "involved in transcription" (which include genes directly or indirectly involved in transcription) based on GO analysis, from the list of genes differentially expressed between murine FL E14.5 and ABM HSCs.[28] This yielded 269 differentially regulated genes, of which, 126 were more highly expressed in FL HSCs and 143 in ABM HSCs (Table S5). Based on literature mining of this gene list, we identified 88 genes with known role in different aspects of hematopoiesis, such as self-renewal and differentiation of HSC, leukemia etc. (Fig. 2A and Table S6). Following removal of genes with known function in hematopoiesis, we identified a list of zebrafish orthologs for 123 of the genes differentially expressed between E14.5 FL and ABM HSCs (Fig. 2B and Table S7). We designed MOs against 18 of these genes, 9 of which were more highly expressed in E14.5 FL HSCs, and 9 in ABM HSCs (Fig. 2B and Table 1). To confirm the differential expression observed by RNA-seq, we performed qRT-PCR on 8 of the genes that were selected for functional validation, and demonstrated consistent increased/decreased gene expression in 3-5 separately isolated FL or ABM HSC populations (Fig. 2C).

In vivo functional screen in Zebrafish identified novel genes with role in hematopoiesis

The MOs were injected at different concentrations in 1-2 cell stage, double transgenic (Tg:gata1;DsRed/flk1;EGFP) zebrafish embryos wherein endothelial cells express EGFP under the *flk1* promoter and erythrocytes express dsRed under the *gata1* promoter. A similar approach was previously used by our group to identify hematopoietic regulators from a gene list created by comparing the global gene expression of primitive HSCs with hematopoietic progenitors from human umbilical cord blood and ABM.[29]

We assessed the presence and circulation of dsRed$^+$ red blood cells and GFP$^+$ endothelial cells at 48hpf by fluorescence microscopy. Five MOs (against *tdg*, *uhrf1, uchl5, nfix*, and *ncoa1*), caused a blood defect with either disruption in blood flow or reduction in gata1:Dsred expressing cells in more than 60% of embryos (Fig. 3A, and Table 1). In addition to blood defects, several other phenotypes, including defects in neural development, abnormalities in vasculature and remodeling of vessels in caudal vein plexus were also seen (Table S8). Injection of 4 MOs (against *taf6l, zbtb20, tle2*, and *pura*) caused early embryonic lethality even when low doses of MOs were injected (Table 1). Injection of the other 9 MOs did not cause any specific hematopoietic defects, while embryos developed normally.

To evaluate the specificity of the MO knockdown, we used a 5-base pair (bp) mismatch control against *uhrf1, tdg* and *uchl5* as well as a splice-blocking MO against *tdg* and *uchl5*. In embryos targeted with mismatch control MOs, we observed no difference in blood and endothelial formation relative to uninjected embryos at 48hpf (Fig. S2A). Knockdown of *tdg* with a splice-blocking MO caused a similar phenotype as observed following injection of the translation-blocking MO (Fig. S2B). By contrast, knockdown of *uchl5* with a splice-blocking MO did not fully recapitulate the decrease in gata1$^+$ cells or blood flow seen with the translation-blocking MO, even if the embryos were curled or bend from the trunk region (Fig. S2B).

To further confirm the effect of the MOs against *tdg, uhrf1, uchl5, and ncoa1* on hematopoiesis, we analyzed the expression levels of transcripts for *lcp1 and hbae1* specific for erythroid and myeloid lineage, respectively, in the MO-treated 48hpf embryos by qRT-PCR (Fig. 3B). These studies demonstrated that MO-based knockdown of *tdg, uhrf1,* and *uchl5* resulted in a significant reduction of transcripts specific for erythroid and myeloid (Fig. 3B). Knockdown of *ncoa1* by contrast, caused no significant change in mature blood cell transcripts.

Knockdown of *tdg*, *uhrf1*, and *ncoa1* inhibit definitive hematopoiesis

We next examined the expression of the definitive hematopoiesis markers *runx1* and *c-myb*,

to assess the effect of the MOs on the emergence of definitive hematopoiesis. Lineage tracing of HSCs during early hematopoietic development demonstrated that expression of *runx1* and *c-myb* appear in the AGM between 28-48 hrs [30,31]. We therefore analyzed the expression of *c-myb* and *runx1* in *tdg, uhrf1, uchl5* and *ncoa1* morphants at 36hpf by whole-mount *in situ* hybridisation (WISH). Based on transcript levels of *c-myb* and *runx1* in different morphants, they were classified as normal, severely decreased and absent expression.

In 80-90% of *tdg, uhrf1* or *ncoa1* morphant embryos, the *c-myb* signal was severely reduced or absent, with loss of *c-myb* signal in 50% of *tdg* and *uhrf1* and 40% of *ncoa1* morphant embryos (Fig. 4A-B). In addition, a severe reduction or absent *runx1* signal was seen in ~80% of *tdg, uhrf1* and *ncoa1* morphants fish (Fig. 5A-B). However, we found fewer morphants fish with complete loss of *runx1* signal compared with *c-myb* signal (Fig. 4A-B). In *uchl5* morphants, we only detected a severe loss of *runx1* signal in 8% of the embryos (Fig. 4A-B). Likewise, reduction of the *c-myb* signal was less pronounced in *uchl5* morphants, where no *c-myb* signal was detected in 20% of the embryos and a severely decreased signal in 30% of embryos (Fig. 4A-B). Noteworthy, when we carefully examined *c-myb* expression in the *uchl5* morphant fish, we detected an accumulation of *c-myb* signal in the posterior blood island (PBI) region (Fig. 4A-B). Thus, these MO knockdown studies demonstrate a role of *tdg, uhrf1* and *ncoa1* in the development of definitive hematopoiesis in the AGM region of zebrafish, whereas loss if *uchl5* caused a less pronounced defect in emergence of definitive hematopoiesis.

Discussion

The function of LTR-HSCs in adult BM differs significantly from those in FL. During development, HSCs populate the FL at around E12.5, following which they expand extensively via symmetrical self-renewing cell divisions between E12.5 and 16.5, while form E16.5 onwards, FL HSCs migrate to the developing BM via the blood circulation. In the fetal BM, expansion of the HSCs continues albeit at a decreased rate, and LT-HSCs ABM loose the fetal HSC characteristics from 4-5 weeks after birth onwards. In the adult BM, LT-HSCs are largely quiescent and divide asymmetrically to generate short-term repopulating (STR) HSCs, which then repopulate the mature cell populations. As the molecular regulators for symmetrical stem cell divisions are yet to be identified, we compared the gene expression profile of LTR-HSCs derived from different FL stages and ABM. We used an RNA-Seq based approach that allows identification of unknown transcripts involved in the processes. As RNA-Seq provides absolute quantification of the levels of expression with significantly lower background noise, identification of subtle transcriptional differences can be captured.

This was clearly the case in this study, as we did not only identify most of the known important hematopoietic regulators, but also several novel regulators. Studies to identify unknown transcripts, non-coding genetic elements as well as alternatively spliced transcripts, involved in the regulation of hematopoietic processes are ongoing. We also observed that differences in the transcriptome of HSCs isolated from FL tissues from different gestational stages were significantly less pronounced, compared with differences observed between the expressed transcriptome of FL and ABM HSCs (data not shown). Further analysis of these subtle differences between the different stages of FL HSC development might identify additional regulators involved in hematopoietic development or HSC function within the FL tissue.

In this study, we focused on differential gene expression between FL14.5 and BM HSCs, stages where HSCs are actively proliferating and remain quiescent, respectively. Two recent studies have used microarray based gene expression analysis to compare the transcriptome

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of LT-HSCs in FL E14.5 and ABM [6,32]. McKinny-Freeman *et al,* who isolated FL HSCs as Lin^- $Sca\text{-}1^+c\text{-}kit^+CD150^+CD48^-$ cells and ABM HSCs as $Lin^-Sca\text{-}1^+c\text{-}kit^+CD150^+CD34^-$ cells, identified 128 differentially expressed genes between FL E14.5 and BM HSC (threshold; $\log_2$FC ≥2, FDR ≤ 0.05)[6]. Among these, 128 differentially expressed genes, 83 genes (~60%) were also found in our list of 576 differentially regulated genes (Fig. S3). In a second study, Beerman *et al.,* who isolated FL HSCs $Lin^-Sca\text{-}1^+c\text{-}kit^+CD150^+CD48^-$ cells and ABM HSCs as $Lin^-Sca\text{-}1^+c\text{-}kit^+CD34^-Flk2^-Il7ra^-$ cells, identified 403 genes differentially expressed between FL and ABM HSCs, among which 147 genes (~35%) were also identified in our dataset (Fig. S3A and S3B,C) [32]. Whether the differences in markers used for HSC isolation might explain the decreased overlap between genes found differentially expressed in our study and the Beerman *et al.,* study is not clear. Nevertheless, significant concordance exists between the three studies.

In this study we focused on the role of transcription regulators, i.e. genes that are directly or indirectly involved in transcription, as these may be major players in the different proliferative behavior of FL and ABM HSCs. Following removal of genes with known function in hematopoiesis, and defining for which transcripts a putative zebrafish orthologue exists, we shortlisted 123 differentially expressed E14.5 FL and ABM HSCs. For 18 genes from this list, MOs were designed to assess the effect on the emergence of HSCs in double transgenic (Tg:gata1;DsRed/flk1;EGFP) *Danio rero* embryos. Injection of 9 of these MOs caused defects in zebrafish larvae.

Embryonic lethality was observed following injection of MOs against *taf6l, Zbtb20, tle2*, and *pura*. Whether they would affect HSC emergence can thus not be defined using this approach. Currently no *taf6l* and *tle2* knockout mice have been described. However, in *X. tropicalis,* the Groucho/TLE family member, *Tle2*, together with *FoxG1* is involved in specification of the ventral telencephalon.[33] Loss of *Zbtb20* in mouse results in severe growth retardation, aberrant glucose metabolism and post-natal lethality.[34] Zbtb20 acts as a transcriptional repressor of alpha-fetoprotein (AFP) and is involved in specification of the CA1 field in developing hippocampus.[35,36] Finally, loss of *Pura* in mouse leads to

death post-natally between d18-28 days, and the mice show significantly decreased numbers of neurons in the hippocampus and cerebellum, indicating its role in brain development.[37]

We also demonstrated that MOs against *tdg*, *uchl5, ncoa1, nfix* and *uchl5* affected the gata-1^+ cell number or circulation at 48hpf. For most MOs, we also identified abnormalities in neural development and vasculature. Combined defects in HSC emergence and vasculature might be due to the fact that hematopoietic and vascular cells originate from a common progenitor, i.e. the hemogenic endothelium. The effects of MOs targeting *tdg* and *nfix* on brain development are consistent with the known roles of these transcriptional regulators in brain development.[38,39]

Aside from assessing the effects of the MOs against *tdg*, *uchl5, ncoa1,* and *uchl5* on *gata-1*$^+$ cells in the zebrafish circulation, we also assessed the emergence of *runx1*$^+$ and *c-myb*$^+$ HSCs by WISH on 36hpf, at which time the definitive HSCs emerge in the AGM. These studies revealed that MOs against *tdg*, *uchl5, ncoa1,* and to a lesser extent *uchl5,* resulted in a significantly lower numbers of HSCs appearing in the ICM. Among these genes, *tdg, uchl5* and *uhrf1* are more highly expressed in FL HSCs while *ncoa1* is more highly expressed in ABM HSCs.

Although myeloid and erythroid specific gene expression as well as the number of *gata-1*$^+$ cells were significantly decreased in *uchl5* morphants, we did not observe significant changes in HSC numbers in the AGM. However, we found an accumulation of *c-myb*$^+$ hematopoietic precursors in the PBI, which represents a region where bipotent erythromyeloid progenitors (EMP) reside temporarily, between 24-36 hpf and marks a transient definitive wave of hematopoiesis which exists between primitive and definitive hematopoiesis.[40] This suggests that *uchl5* may be important for the differentiation of EMPs, causing their accumulation with concomitant loss of mature blood cells. UCHL5 is a deubiquitinating enzyme, which can reverse Smurf-mediated ubiquitination of Smad transcription factors,[41] known to play important roles in hematopoietic development, as

well as in postnatal HSCs. *Uchl5* knockout mice die prenatally, because of severe defects in brain development[42].

The *ncoa1* morphants were the only ones wherein mature blood cell marker expression was not affected, even if HSCs in the AGM were decreased. Ncoa1 is known to play a role in chromatin remodeling through the recruitment of other coactivators. *Ncoa1* knockout mice show a partial resistance to sex steroid hormones, affecting the reproductive system, the skeleton, glucose production [43] and has a role in the development of Purkinje cells in the brain, resulting in moderate motor dysfunction [44]. Why loss of *ncoa1* expression decreases the number of *c-myb/runx1*$^{+}$ HSCs in the AGM of zebrafish larvae, even though it is more highly expressed in the ABM, will need to be further investigated.

Knockdown of *tdg* and *uhrf1* had profound effects on the development of the hematopoietic system at 48hpf (as demonstrated by lack of circulating blood, and severely decreased expression of *runx1* and *c-myb* mRNA). TDG and UHRF1 play important roles in DNA methylation, as well as in DNA repair. Tdg is one of the enzymes that starts base excision repair (BER), which corrects among others damage to the DNA by oxidation; while Uhrf1 plays a role in DSBR [45-47]. We recently reported significantly higher expression in the expression of OxPhos genes in FL compared with BM HSCs, which was accompanied with presence of significantly more and more active mitochondria, increased oxygen consumption rate and increased ROS levels in FL HSCs compared with BM HSCs [23]. KEGG pathway analysis also demonstrated that all DNA repair pathways were significantly more enriched in FL compared to BM HSCs. We speculate that this may be required for FL HSCs to be capable to deal with the significantly higher ROS levels, known to cause DNA damage, and HSC exhaustion. In line with this hypothesis, we found that MO knockdown of two genes involved in DNA repair, namely *Tdg* and *Uhrf1* caused significant hematopoietic toxicity in the zebrafish model. Knockout of *Tdg* and *Uhrf1* in mice is associated with embryonic lethality [48] / early gestational death [49]; therefore their effect on mammalian hematopoiesis remains unevaluated. Lineage specific knockout studies or shRNA mediated inhibition of both genes in HSCs will be required to address if *Tdg* and *Uhrf1* affect HSC in

mammals.

In conclusion, we identified 3 new hematopoietic regulators that affect the emergence and/or proliferation of definitive HSCs in zebrafish. It will obviously be of interest to demonstrate in future studies that knockdown or overexpression of these regulators in mammalian HSCs can increase HSC expansion.

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Figure Legends:

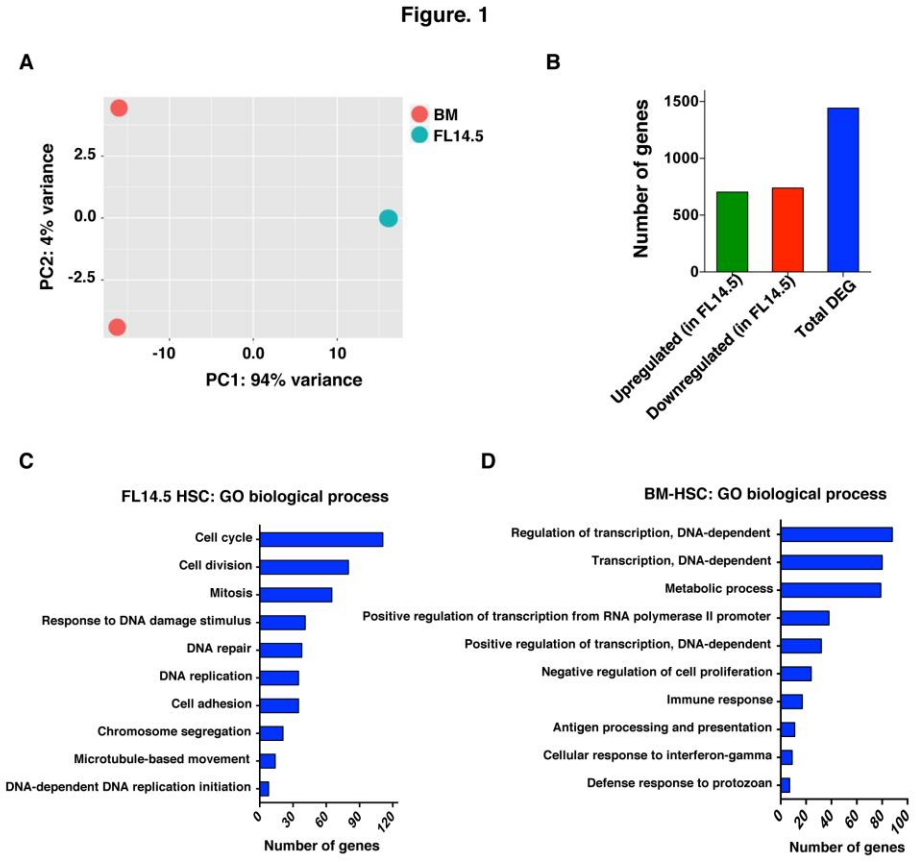

Figure 1. Genome-scale transcriptional profiling between murine FL and ABM LT-HSC.

A. RNASeq analysis was performed as described in an earlier publication [23]. Principle component analysis across different cell populations.

B. Number of differentially regulated genes obtained after pair-wise comparison between LT-HSCs from murine FL E14.5 and adult BM. Threshold used is: Log2FC ≥ 1 FDR ≤ 0.05.

C-D. Gene set enrichment analysis for GO biological process for genes differentially expressed between murine FL E14.5 and ABM HSCs using the web-based application Genecodis3.

Figure. 2

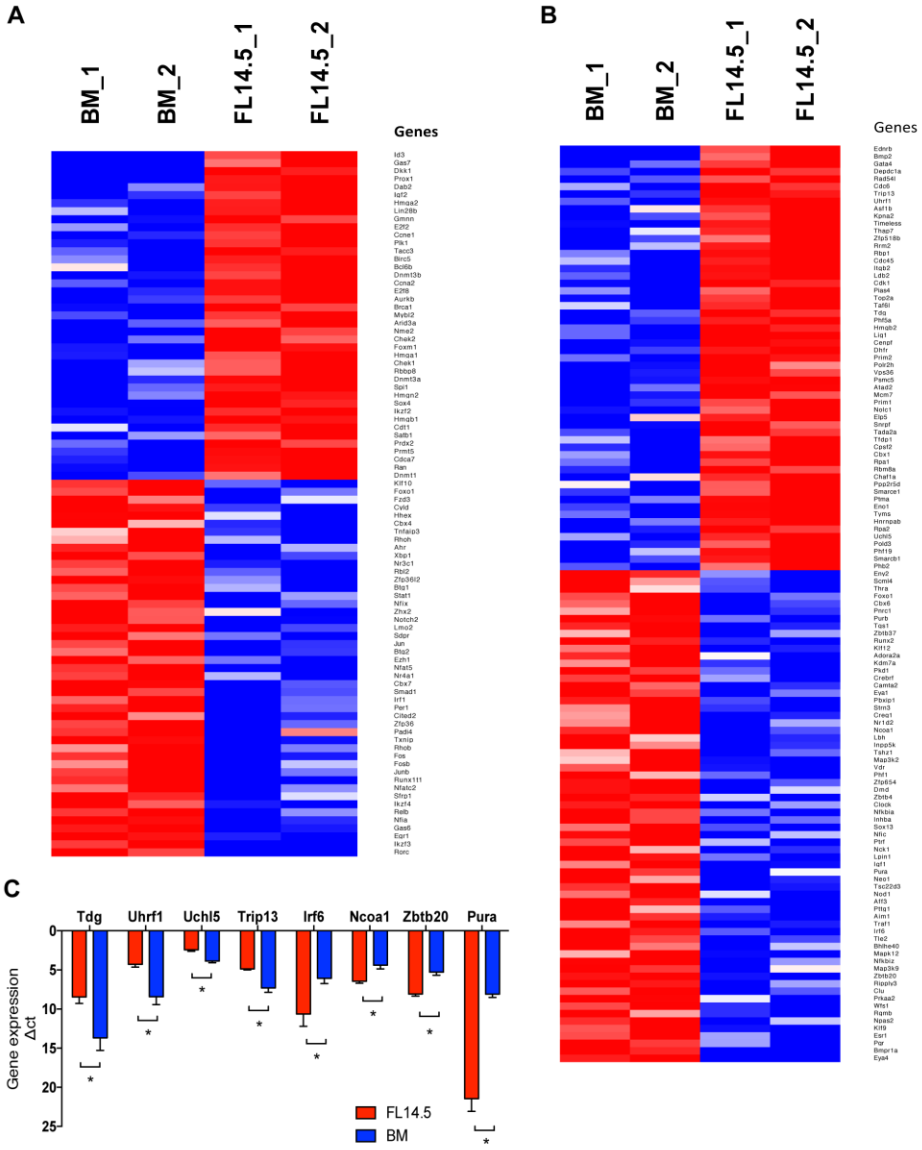

Figure 2. Shortlisting of genes differentially regulated between murine E14.5 FL and ABM.

A. Heat map of shortlisted differentially expressed genes selected on basis of the GO annotation (Biological process: transcription) and with known role in HSC function.

B. Heat map of shortlisted differentially expressed gene selected on basis of the GO annotation (Biological process: transcription) and having zebrafish ortholog with no known role in regulation of HSC function between FL14.5 and ABM LT-HSC.

C. Representative differentially expressed genes confirmed by qRT-PCR. (n=3-6; *t* test, * p-value ≤ 0.05)

Figure. 3

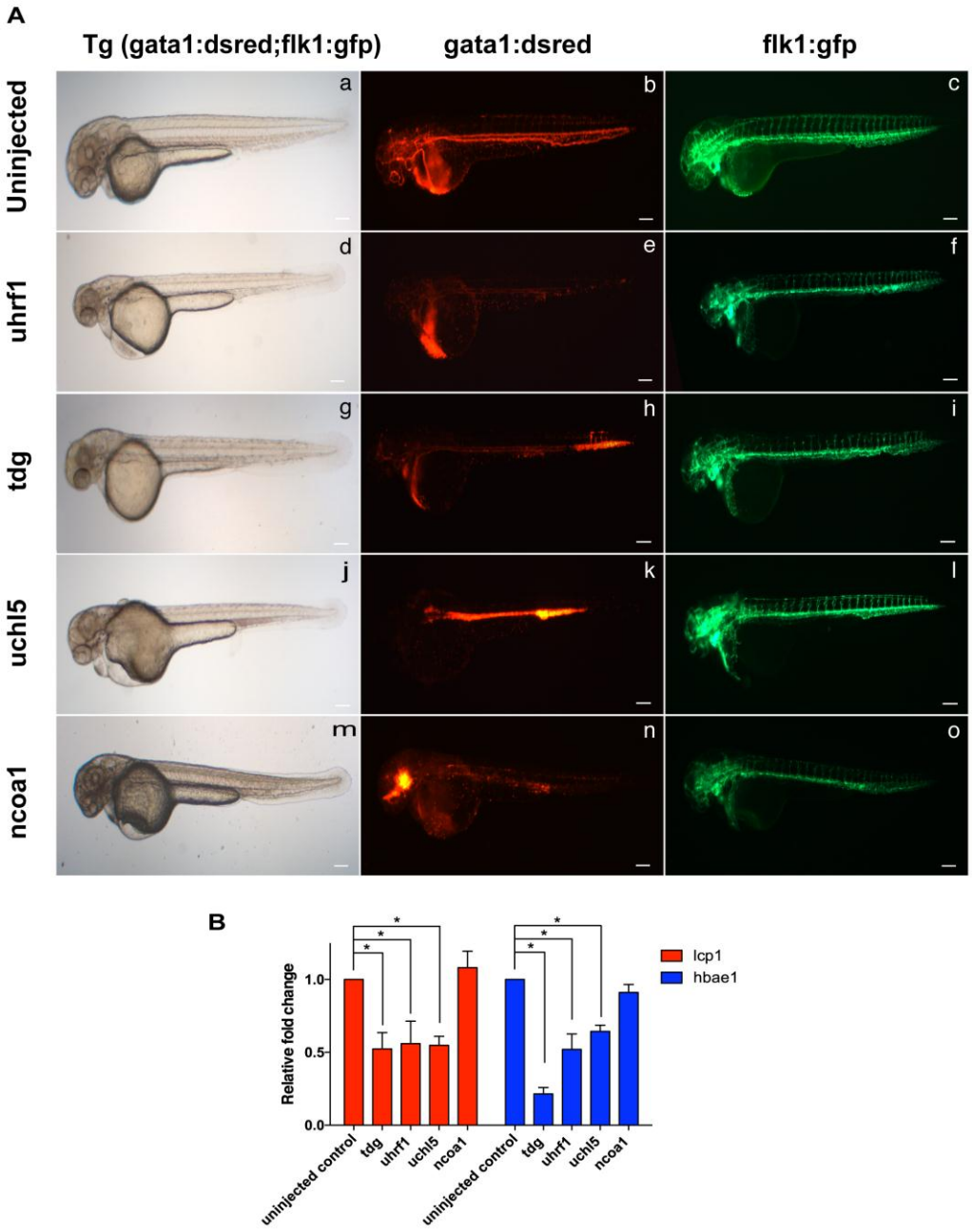

Figure 3. Morpholino knockdown of target genes in Tg:gata1;DsRed/flk1;EGFP zebrafish.

A. Representative fluorescence images of embryos (48 hpf): (a-b) uninjected control; and after injection of MOs against *uhrf1* (d-f), *tdg* (g-i), *uchl5* (j-i), and *ncoa1*(m-o).

B. Gene expression of *lcp1* (myeloid specific) and *hbae1* (erythroid specific) in MO injected embryos relative to uninjected controls at 48hpf. (n= 4-6 (1replicate=3 x 6 embryos), *t* test, * p-value ≤ 0.05).

Figure. 4

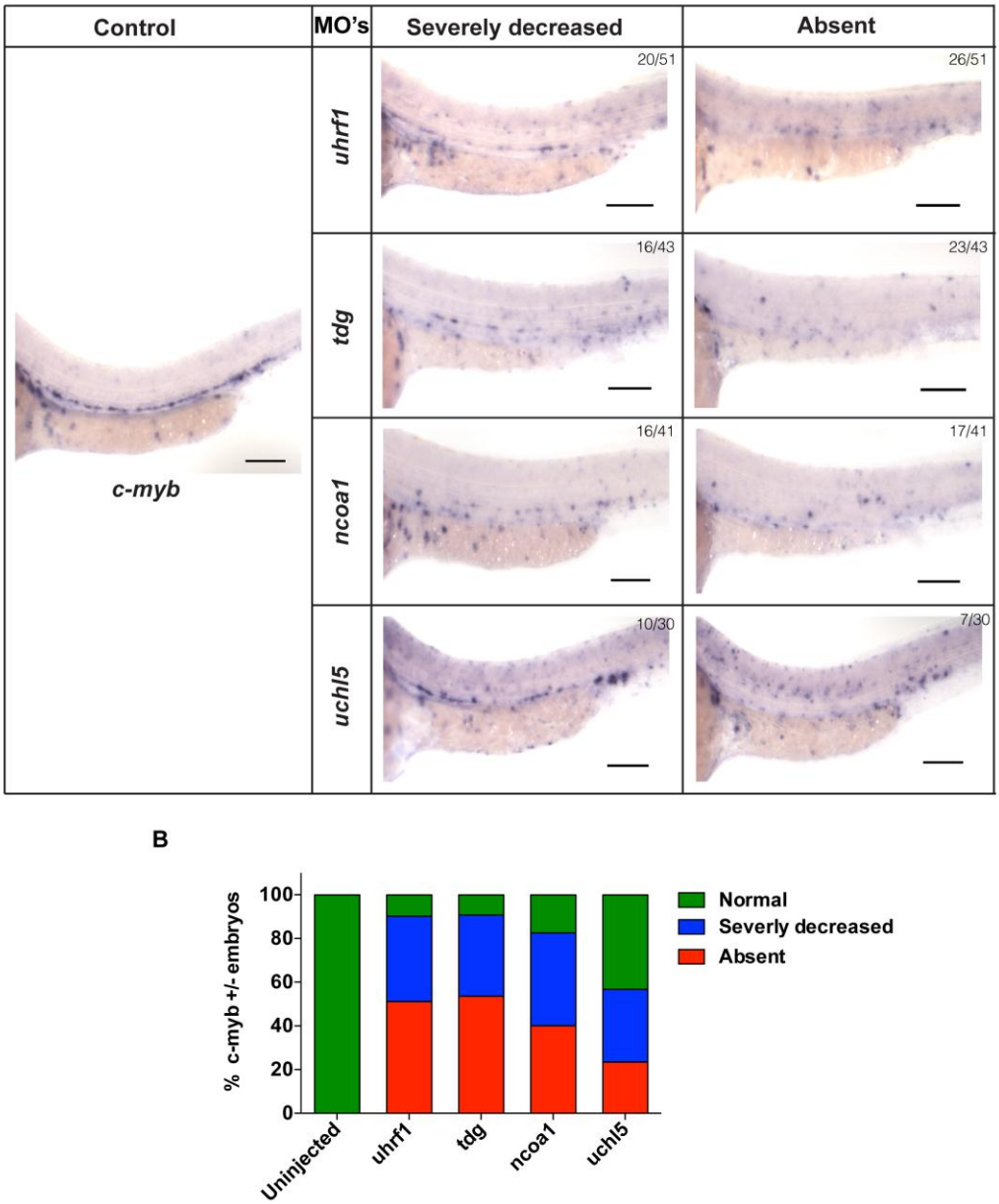

Figure 4. Expression of *c-myb* in control and morpholino targeted embryos by WISH.

A. Representative *in situ* image of *c-myb* expression in uninjected control embryos and embryos injected with MOs against *uhrf1, tdg, ncoa1,* and *uchl5*.

B. Quantification of embryos with different degrees of *c-myb* expression following injection with MOs against *uhrf1, tdg, ncoa1,* and *uchl5*.

Figure. 5

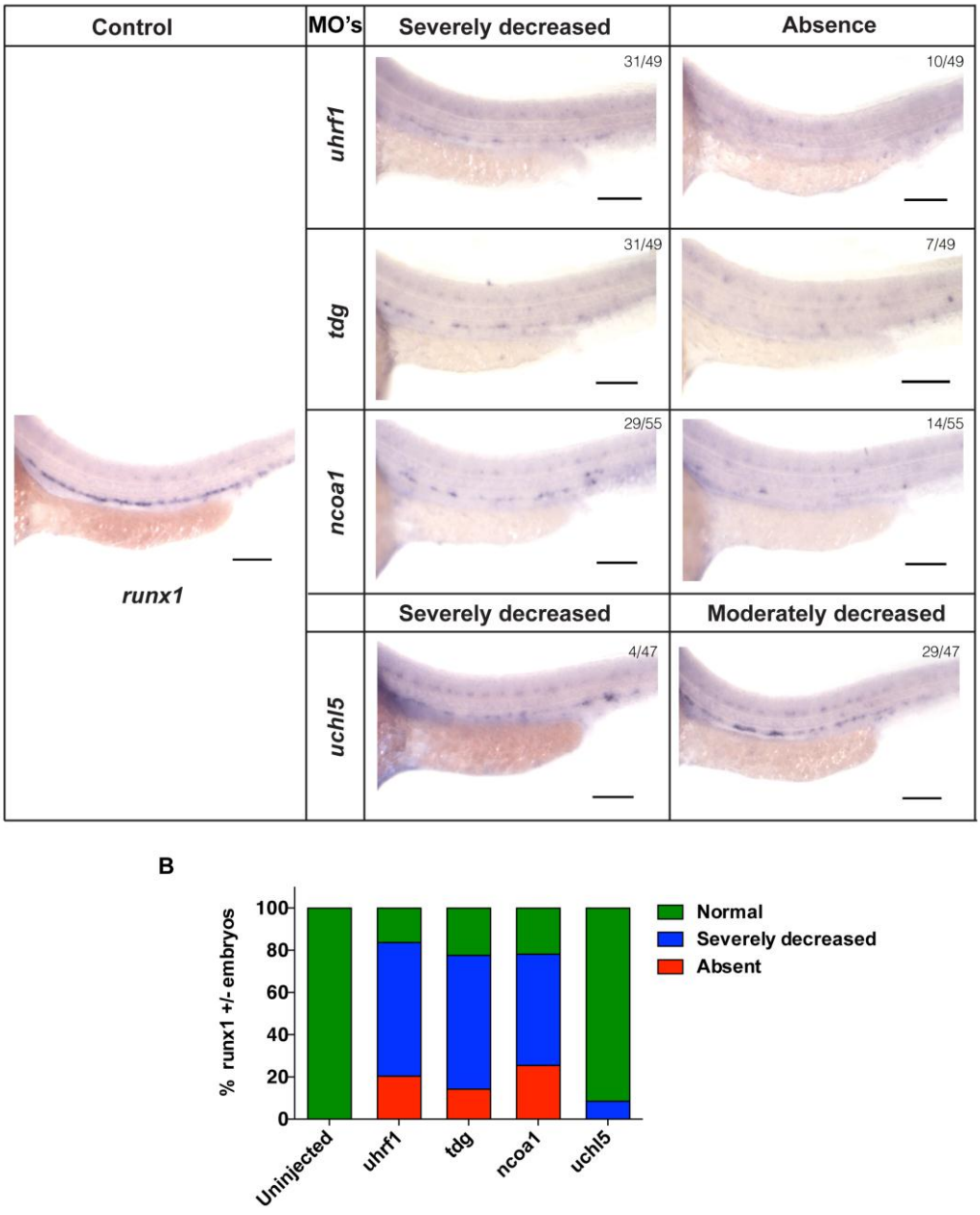

Figure 5. Expression of *runx1* in control and morpholino targeted embryos by WISH.

A. Representative *in situ* image of *runx1* expression in uninjected control embryos and embryos injected with MOs against *uhrf1, tdg, ncoa1,* and *uchl5*.

B. Quantification of embryos with different degrees of *runx1* expression following injection with MOs against *uhrf1, tdg, ncoa1,* and *uchl5*.

Gene Symbol	MO translational/splice	Dose	Hematopoietic Phenotype	Expression
Uchl5	ATG / Splice morpholino	4 ng	~60% of embryos showed blood defect	FL14.5
Uhrf1	ATG morpholino	3 ng	~60-70% of embryos showed blood defect	FL14.5
Tdg	ATG / Splice morpholino	6 ng	~70% of embryos showed blood defect	FL14.5
Taf6l	ATG morpholino	1.5 ng	Embryonic Lethal	FL14.5
Thap7	ATG morpholino	6 ng	No blood defect	FL14.5
Timeless	ATG morpholino	6 ng	No blood defect	FL14.5
Trip13	ATG morpholino	6 ng	No blood defect	FL14.5
Depdc1a	ATG morpholino	6 ng	No blood defect	FL14.5
Tada2a	ATG morpholino	6 ng	No blood defect	FL14.5
Nfix	ATG morpholino	3ng	~60% of embryos showed blood defect	BM
Ncoa1	ATG morpholino	4.5 ng	~70% embryo showed blood defec	BM
Zbtb20	ATG morpholino	2 ng	Embryonic Lethal	BM
Tle2	ATG morpholino	1.5 ng	Embryonic Lethal	BM
Pura	ATG morpholino	1.5 ng	Embryonic Lethal	BM
Lpin1	ATG morpholino	6 ng	No blood defect	BM
Tsc22d3	ATG morpholino	6 ng	No blood defect	BM
Irf6	ATG morpholino	6 ng	No blood defect	BM
Bhlhe40	ATG morpholino	6 ng	No blood defect	BM

Table1. Morpholino knockdown of shortlisted candidate genes.

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Supplementary figure legends:

Figure. S1: Mapping statistics and correlation analysis after RNA-Seq for LT-HSC from murine FLs and BM: A) Percentages of reads mapped to reference genome after RNA-seq analysis performed on murine FL E14.5 and adults BM LT-HSCs. **B)** A percentage of reads mapped to genes after RNA-seq analysis performed on FL E14.5 and adults BM LT-HSCs. **C)** The correlation coefficients between replicates of different samples derived from FL E14.5 and adults BM LT-HSCs.

Figure. S2: Morpholino knockdown of target genes in Tg:gata1;DsRed/flk1;EGFP zebrafish line: A) Representative fluorescence images of embryos (48 hpf): (a-c) uninjected control; after injection of 5-base pair (bp) mismatch control MOs against *uhrf1* (d-f), *tdg* (g-i) and *uchl5* (j-l). **B)** Representative fluorescence images of embryos (48 hpf): (a-c) uninjected control; after injection of splice-blocking MOs against *tdg* (d-f) and *uchl5* (g-i).

Figure. S3: Cross-comparison of RNA-seq with published microarray dataset:

A. Comparison of differentially expressed genes in this study with results from McKinny-Freeman *et al.,* and Beerman *et al.,* [6,32]. Venn diagram depicting the overlap of differentially regulated genes in these three independent studies. Threshold used is: Log2FC ≥2, FDR ≤0.05. **B)** Comparison of differentially expressed genes in this study with results from McKinny-Freeman *et al.,* and Beerman *et al.,* [6,32]. Depicted is the number of genes differentially expressed between FL E14.5 and BM in the three independent studies and overlap estimated after cross-comparison

of differential gene expression. **C)** Description of cell surface markers used for purification of LT-HSC from E14.5 FL and adult bone marrow in McKinny-Freeman *et al.,* and Beerman *et al.,* [6,32].

Figure. S1

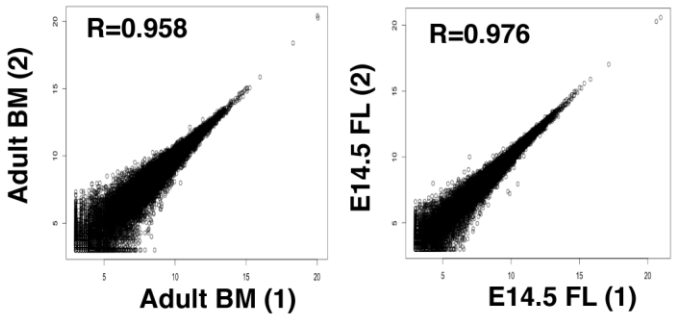
A.

Sample	Total reads	Reads mapped to Genome			
		No. of reads	% of total reads	Unique match	% of total reads
FL14.5-1	39541158	34835501	88.10%	33049926	83.58%
FL14.5-2	38343180	34099745	88.93%	32464103	84.67%
BM1	39119372	35566226	90.92%	34248275	87.55%
BM2	38640484	34805547	90.08%	33451360	86.57%

B.

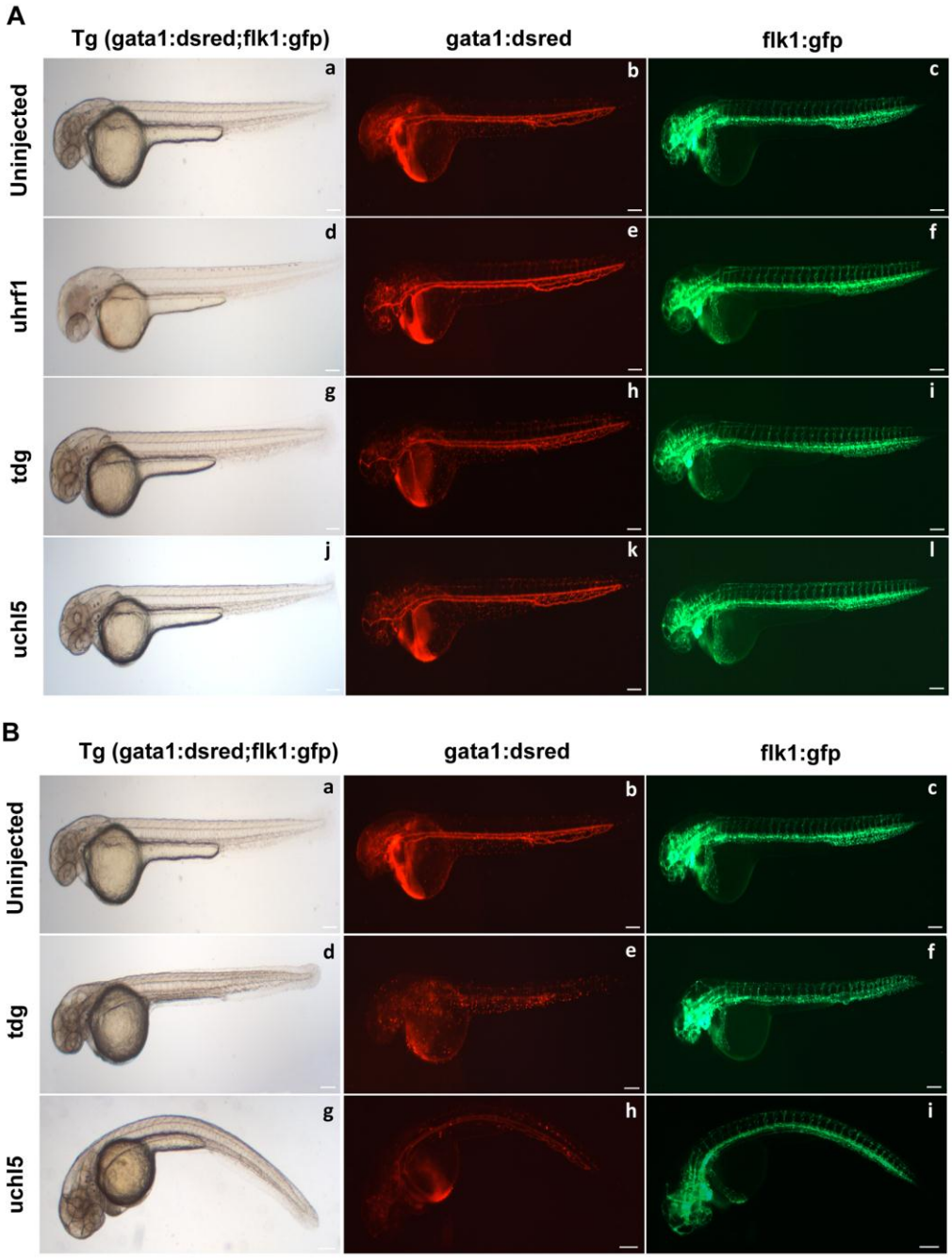
Sample	Total reads	Reads mapped to Genes			
		No. of reads	% of total reads	Unique match	% of total reads
FL14.5-1	39541158	15014048	37.97%	14527732	36.74%
FL14.5-2	38343180	15000015	39.12%	14517561	37.86%
BM1	39119372	12021107	30.73%	11611807	29.68%
BM2	38640484	12544338	32.46%	12143640	31.43%

C.



Mapping statistics and correlation analysis after RNA-Seq for LT-HSC from murine FLs and BM

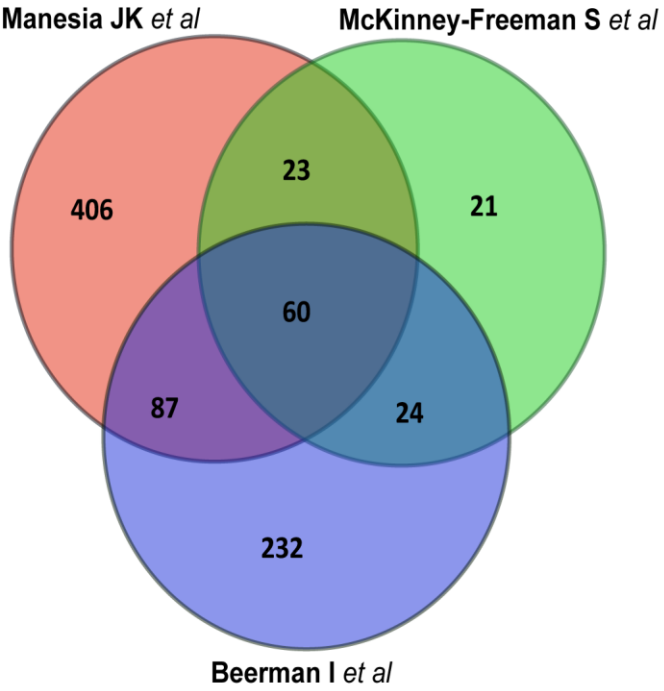
Figure. S2



Morpholino knockdown of target genes in Tg:gata1;DsRed/flk1;EGFP zebrafish line

Figure. S3

A



B

	Overlapping of differential expresed genes (DEG)		
	Manesia JK et al	McKinney-Freeman S	Overlap
No. of DEG	576	128	83
	Manesia J et al	Beerman I et al	Overlap
No. of DEG	576	403	147

Threshold: Log2FC ≥ 2, FDR ≤ 0.05

C

HSC source	Population	Cell surface phenotype	Reference	Accession NO.
Adult BM	LT-HSC	Lin-Sca-1+c-kit+CD150+CD34-	McKinney-Freeman S et al, 2012	GSE37000
FL E14.5	LT-HSC	Lin-Sca-1+c-kit+CD150+CD48-		
Adult BM	LT-HSC	Lin-Sca-1+c-kit+ CD34- Flk2- Il7ra-	Beerman I et al, 2014	GSE55525
FL E14.5	FL HSC	Lin-Sca-1+c-kit+ CD150+CD48-		

Cross-comparison of RNA-seq with published microarray dataset

table s1. qrt-pcr primer sequences.xlsx

table s2. morpholino list.xlsx

table s3. all gene coverage and rpkm.xlsx

Distinct molecular signature of murine fetal liver and adult hematopoietic stem cells identifies novel regulators of hematopoietic stem cell function (doi: 10.1089/scd.2016.0294)
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table s4. pair-wise comparion hsc from e14.5 and bm.xlsx

table s5. go biological process trancription.xlsx

Distinct molecular signature of murine fetal liver and adult hematopoietic stem cells identifies novel regulators of hematopoietic stem cell function (doi: 10.1089/scd.2016.0294)
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table s6. gene with known role in hsc self-renewal or hematopoiesis.xlsx

table s7. genes with unknown role in hematopoiesis with zebrafish orthologs.xlsx

table s8. detail phenotype after mo knockdown.xlsx